

Just
A.

SEQUENCE LISTING

<110> Japan Science and Technology Corporation,
and Harumi SAKAI

<120> Monoclonal antibodies against human apoptosis inhibitory protein NAIP,
and method for assaying the NAIP

<130> 99-F-051PCT/YS

<140> PCT/JP99/05841

<141> 1999-10-22

<150> JP No. 10-304550

<151> 1998-10-26

<160> 2

<210> 1

<211> 1403

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Thr Gln Gln Lys Ala Ser Asp Glu Arg Ile Ser Gln Phe Asp

1 5 10 15

His Asn Leu Leu Pro Glu Leu Ser Ala Leu Leu Gly Leu Asp Ala Val

20 25 30

Gln Leu Ala Lys Glu Leu Glu Glu Glu Gln Lys Glu Arg Ala Lys

35 40 45

Met Gln Lys Gly Tyr Asn Ser Gln Met Arg Ser Glu Ala Lys Arg Leu

50 55 60

Lys Thr Phe Val Thr Tyr Glu Pro Tyr Ser Ser Trp Ile Pro Gln Glu

65 70 75 80

Met Ala Ala Ala Gly Phe Tyr Phe Thr Gly Val Lys Ser Gly Ile Gln

85 90 95

09830338-071101

Cys	Phe	Cys	Cys	Ser	Leu	Ile	Leu	Phe	Gly	Ala	Gly	Leu	Thr	Arg	Leu
100				105				110							
Pro	Ile	Glu	Asp	His	Lys	Arg	Phe	His	Pro	Asp	Cys	Gly	Phe	Leu	Leu
115				120				125							
Asn	Lys	Asp	Val	Gly	Asn	Ile	Ala	Lys	Tyr	Asp	Ile	Arg	Val	Lys	Asn
130				135				140							
Leu	Lys	Ser	Arg	Leu	Arg	Gly	Gly	Lys	Met	Arg	Tyr	Gln	Glu	Glu	Glu
145				150				155				160			
Ala	Arg	Leu	Ala	Ser	Phe	Arg	Asn	Trp	Pro	Phe	Tyr	Val	Gln	Gly	Ile
165				170				175							
Ser	Pro	Cys	Val	Leu	Ser	Glu	Ala	Gly	Phe	Val	Phe	Thr	Gly	Lys	Gln
180				185				190							
Asp	Thr	Val	Gln	Cys	Phe	Ser	Cys	Gly	Gly	Cys	Leu	Gly	Asn	Trp	Glu
195				200				205							
Glu	Gly	Asp	Asp	Pro	Trp	Lys	Glu	His	Ala	Lys	Trp	Phe	Pro	Lys	Cys
210				215				220							
Glu	Phe	Leu	Arg	Ser	Lys	Lys	Ser	Ser	Glu	Glu	Ile	Thr	Gln	Tyr	Ile
225				230				235				240			
Gln	Ser	Tyr	Lys	Gly	Phe	Val	Asp	Ile	Thr	Gly	Glu	His	Phe	Val	Asn
245				250				255							
Ser	Trp	Val	Gln	Arg	Glu	Leu	Pro	Met	Ala	Ser	Ala	Tyr	Cys	Asn	Asp
260				265				270							
Ser	Ile	Phe	Ala	Tyr	Glu	Glu	Leu	Arg	Leu	Asp	Ser	Phe	Lys	Asp	Trp
275				280				285							
Pro	Arg	Glu	Ser	Ala	Val	Gly	Val	Ala	Ala	Leu	Ala	Lys	Ala	Gly	Leu
290				295				300							
Phe	Tyr	Thr	Gly	Ile	Lys	Asp	Ile	Val	Gln	Cys	Phe	Ser	Cys	Gly	Gly
305				310				315				320			

Cys Leu Glu Lys Trp Gln Glu Gly Asp Asp Pro Leu Asp Asp His Thr
 325 330 335
 Arg Cys Phe Pro Asn Cys Pro Phe Leu Gln Asn Met Lys Ser Ser Ala
 340 345 350
 Glu Val Thr Pro Asp Leu Gln Ser Arg Gly Glu Leu Cys Glu Leu Leu
 355 360 365
 Glu Thr Thr Ser Glu Ser Asn Leu Glu Asp Ser Ile Ala Val Gly Pro
 370 375 380
 Ile Val Pro Glu Met Ala Gln Gly Glu Ala Gln Trp Phe Gln Glu Ala
 385 390 395 400
 Lys Asn Leu Asn Glu Gln Leu Arg Ala Ala Tyr Thr Ser Ala Ser Phe
 405 410 415
 Arg His Met Ser Leu Leu Asp Ile Ser Ser Asp Leu Ala Thr Asp His
 420 425 430
 Leu Leu Gly Cys Asp Leu Ser Ile Ala Ser Lys His Ile Ser Lys Pro
 435 440 445
 Val Gln Glu Pro Leu Val Leu Pro Glu Val Phe Gly Asn Leu Asn Ser
 450 455 460
 Val Met Cys Val Glu Gly Glu Ala Gly Ser Gly Lys Thr Val Leu Leu
 465 470 475 480
 Lys Lys Ile Ala Phe Leu Trp Ala Ser Gly Cys Cys Pro Leu Leu Asn
 485 490 495
 Arg Phe Gln Leu Val Phe Tyr Leu Ser Leu Ser Ser Thr Arg Pro Asp
 500 505 510
 Glu Gly Leu Ala Ser Ile Ile Cys Asp Gln Leu Leu Glu Lys Glu Gly
 515 520 525
 Ser Val Thr Glu Met Cys Met Arg Asn Ile Ile Gln Gln Leu Lys Asn
 530 535 540

09820338-0740

Gln Val Leu Phe Leu Leu Asp Asp Tyr Lys Glu Ile Cys Ser Ile Pro
 545 550 555 560
 Gln Val Ile Gly Lys Leu Ile Gln Lys Asn His Leu Ser Arg Thr Cys
 565 570 575
 Leu Leu Ile Ala Val Arg Thr Asn Arg Ala Arg Asp Ile Arg Arg Tyr
 580 585 590
 Leu Glu Thr Ile Leu Glu Ile Lys Ala Phe Pro Phe Tyr Asn Thr Val
 595 600 605
 Cys Ile Leu Arg Lys Leu Phe Ser His Asn Met Thr Arg Leu Arg Lys
 610 615 620
 Phe Met Val Tyr Phe Gly Lys Asn Gln Ser Leu Gln Lys Ile Gln Lys
 625 630 635 640
 Thr Pro Leu Phe Val Ala Ala Ile Cys Ala His Trp Phe Gln Tyr Pro
 645 650 655
 Phe Asp Pro Ser Phe Asp Asp Val Ala Val Phe Lys Ser Tyr Met Glu
 660 665 670
 Arg Leu Ser Leu Arg Asn Lys Ala Thr Ala Glu Ile Leu Lys Ala Thr
 675 680 685
 Val Ser Ser Cys Gly Glu Leu Ala Leu Lys Gly Phe Phe Ser Cys Cys
 690 695 700
 Phe Glu Phe Asn Asp Asp Asp Leu Ala Glu Ala Gly Val Asp Glu Asp
 705 710 715 720
 Glu Asp Leu Thr Met Cys Leu Met Ser Lys Phe Thr Ala Gln Arg Leu
 725 730 735
 Arg Pro Phe Tyr Arg Phe Leu Ser Pro Ala Phe Gln Glu Phe Leu Ala
 740 745 750
 Gly Met Arg Leu Ile Glu Leu Leu Asp Ser Asp Arg Gln Glu His Gln
 755 760 765

09830338-074404
 TOTAL 8520360

Asp Leu Gly Leu Tyr His Leu Lys Gln Ile Asn Ser Pro Met Met Thr

770

775

780

Val Ser Ala Tyr Asn Asn Phe Leu Asn Tyr Val Ser Ser Leu Pro Ser

785

790

795

800

Thr Lys Ala Gly Pro Lys Ile Val Ser His Leu Leu His Leu Val Asp

805

810

815

Asn Lys Glu Ser Leu Glu Asn Ile Ser Glu Asn Asp Asp Tyr Leu Lys

820

825

830

His Gln Pro Glu Ile Ser Leu Gln Met Gln Leu Leu Arg Gly Leu Trp

835

840

845

Gln Ile Cys Pro Gln Ala Tyr Phe Ser Met Val Ser Glu His Leu Leu

850

855

860

Val Leu Ala Leu Lys Thr Ala Tyr Gln Ser Asn Thr Val Ala Ala Cys

865

870

875

880

Ser Pro Phe Val Leu Gln Phe Leu Gln Gly Arg Thr Leu Thr Leu Gly

885

890

895

Ala Leu Asn Leu Gln Tyr Phe Phe Asp His Pro Glu Ser Leu Ser Leu

900

905

910

Leu Arg Ser Ile His Phe Pro Ile Arg Gly Asn Lys Thr Ser Pro Arg

915

920

925

Ala His Phe Ser Val Leu Glu Thr Cys Phe Asp Lys Ser Gln Val Pro

930

935

940

Thr Ile Asp Gln Asp Tyr Ala Ser Ala Phe Glu Pro Met Asn Glu Trp

945

950

955

960

Glu Arg Asn Leu Ala Glu Lys Glu Asp Asn Val Lys Ser Tyr Met Asp

965

970

975

Met Gln Arg Arg Ala Ser Pro Asp Leu Ser Thr Gly Tyr Trp Lys Leu

980

985

990

09830338-071101

Ser Pro Lys Gln Tyr Lys Ile Pro Cys Leu Glu Val Asp Val Asn Asp
 995 1000 1005
 Ile Asp Val Val Gly Gln Asp Met Leu Glu Ile Leu Met Thr Val Phe
 1010 1015 1020
 Ser Ala Ser Gln Arg Ile Glu Leu His Leu Asn His Ser Arg Gly Phe
 1025 1030 1035 1040
 Ile Glu Ser Ile Arg Pro Ala Leu Glu Leu Ser Lys Ala Ser Val Thr
 1045 1050 1055
 Lys Cys Ser Ile Ser Lys Leu Glu Leu Ser Ala Ala Glu Gln Glu Leu
 1060 1065 1070
 Leu Leu Thr Leu Pro Ser Leu Glu Ser Leu Glu Val Ser Gly Thr Ile
 1075 1080 1085
 Gln Ser Gln Asp Gln Ile Phe Pro Asn Leu Asp Lys Phe Leu Cys Leu
 1090 1095 1100
 Lys Glu Leu Ser Val Asp Leu Glu Gly Asn Ile Asn Val Phe Ser Val
 1105 1110 1115 1120
 Ile Pro Glu Glu Phe Pro Asn Phe His His Met Glu Lys Leu Leu Ile
 1125 1130 1135
 Gln Ile Ser Ala Glu Tyr Asp Pro Ser Lys Leu Val Lys Leu Ile Gln
 1140 1145 1150
 Asn Ser Pro Asn Leu His Val Phe His Leu Lys Cys Asn Phe Phe Ser
 1155 1160 1165
 Asp Phe Gly Ser Leu Met Thr Met Leu Val Ser Cys Lys Lys Leu Thr
 1170 1175 1180
 Glu Ile Lys Phe Ser Asp Ser Phe Phe Gln Ala Val Pro Phe Val Ala
 1185 1190 1195 1200
 Ser Leu Pro Asn Phe Ile Ser Leu Lys Ile Leu Asn Leu Glu Gly Gln
 1205 1210 1215

0983038-01401
 TTT 20-88808860

Gln Phe Pro Asp Glu Glu Thr Ser Glu Lys Phe Ala Tyr Ile Leu Gly
 1220 1225 1230
 Ser Leu Ser Asn Leu Glu Glu Leu Ile Leu Pro Thr Gly Asp Gly Ile
 1235 1240 1245
 Tyr Arg Val Ala Lys Leu Ile Ile Gln Gln Cys Gln Gln Leu His Cys
 1250 1255 1260
 Leu Arg Val Leu Ser Phe Phe Lys Thr Leu Asn Asp Asp Ser Val Val
 1265 1270 1275 1280
 Glu Ile Ala Lys Val Ala Ile Ser Gly Gly Phe Gln Lys Leu Glu Asn
 1285 1290 1295
 Leu Lys Leu Ser Ile Asn His Lys Ile Thr Glu Glu Gly Tyr Arg Asn
 1300 1305 1310
 Phe Phe Gln Ala Leu Asp Asn Met Pro Asn Leu Gln Glu Leu Asp Ile
 1315 1320 1325
 Ser Arg His Phe Thr Glu Cys Ile Lys Ala Gln Ala Thr Thr Val Lys
 1330 1335 1340
 Ser Leu Ser Gln Cys Val Leu Arg Leu Pro Arg Leu Ile Arg Leu Asn
 1345 1350 1355 1360
 Met Leu Ser Trp Leu Leu Asp Ala Asp Asp Ile Ala Leu Leu Asn Val
 1365 1370 1375
 Met Lys Glu Arg His Pro Gln Ser Lys Tyr Leu Thr Ile Leu Gln Lys
 1380 1385 1390
 Trp Ile Leu Pro Phe Ser Pro Ile Ile Gln Lys
 1395 1400 1403

<210> 2

<211> 5984

<212> DNA

09830338-07404

<213> Homo sapiens

<220>

<221> CDC

<222> (292).. (4500)

<400> 2

ACAAAGGTC CTGTGCTCAC CTGGGACCCT TCTGGACGTT GCCCTGTGTT CCTCTTCGCC 60
 TGCCTGTTCA TCTACGACGA ACCCCGGGTA TTGACCCAG ACAACAATGC CACTTCATAT 120
 TGGGGACTTC GTCTGGGATT CCAAGGTGCA TTCATTGCAA AGTTCCTTAA ATATTTTCTC 180
 ACTGCTTCCT ACTAAAGGAC GGACAGAGCA TTTGTTCTTC AGCCACATAC TTTCTTCCA 240
 CTGGCCAGCA TTCTCCTCTA TTAGACTAGA ACTGTGGATA AACCTCAGAA AATGGCCACC 300
 CAGCAGAAAG CCTCTGACGA GAGGATCTCC CAGTTTGATC ACAATTTGCT GCCAGAGCTG 360
 TCTGCTCTTC TGGGCCTAGA TGCAGTTCAG TTGGCAAAGG AACTAGAAGA AGAGGAGCAG 420
 AAGGAGCGAG CAAAAATGCA GAAAGGCTAC AACTCTCAA TGGCAGTGA AGCAAAAAGG 480
 TTAAAGACTT TTGTGACTTA TGAGCCGTAC AGCTCATGGA TACCACAGGA GATGGCGGCC 540
 GCTGGGTTTT ACTTCACTGG GGTAAATCT GGGATTCACT GCTTCTGCTG TAGCCTAATC 600
 CTCTTTGGTG CCGGCCTCAC GAGACTCCCC ATAGAAGACC ACAAGAGGTT TCATCCAGAT 660
 TGTGGGTTCC TTTTGAACAA GGATGTTGGT AACATTGCCA AGTACGACAT AAGGGTGAAG 720
 AATCTGAAGA GCAGGCTGAG AGGAGGTAAA ATGAGGTACC AAGAAGAGGA GGCTAGACTT 780
 GCATCCTTCA GGAAGTGGCC ATTTTATGTC CAAGGGATAT CCCCTTGTGT GCTCTCAGAG 840
 GCTGGCTTTG TCTTTACAGG TAAACAGGAC ACGGTACAGT GTTTTTCCTG TGGTGGATGT 900
 TTAGGAAATT GGAAGAAGG AGATGATCCT TGAAGGAAC ATGCCAAATG GTTCCCCAAA 960
 TGTGAATTC TTCGGAGTAA GAAATCCTCA GAGGAAATTA CCCAGTATAT TCAAAGCTAC 1020
 AAGGGATTTG TTGACATAAC GGGAGAACAT TTTGTGAATT CCTGGGTCCA GAGAGAATTA 1080
 CCTATGGCAT CAGCTTATTG CAATGACAGC ATCTTTGCTT ACGAAGAACT ACGGCTGGAC 1140
 TCTTTTAAGG ACTGGCCCCG GGAATCAGCT GTGGGAGTTG CAGCACTGGC CAAAGCAGGT 1200
 CTTTTCTACA CAGGTATAAA GGACATCGTC CAGTGCTTTT CCTGTGGAGG GTGTTTAGAG 1260
 AAATGGCAGG AAGGTGATGA CCCATTAGAC GATCACACCA GATGTTTTCC CAATTGTCCA 1320
 TTTCTCCAAA ATATGAAGTC CTCTGCGGAA GTGACTCCAG ACCTTCAGAG CCGTGGTGAA 1380

09830338.01401

090303.0740
TOT 20.8502850

CTTTGTGAAT TACTGGAAAC CACAAGTGAA AGCAATCTTG AAGATTCAAT AGCAGTTGGT	1440
CCTATAGTGC CAGAAATGGC ACAGGGTGAA GCCCAGTGGT TTCAAGAGGC AAAGAATCTG	1500
AATGAGCAGC TGAGAGCAGC TTATACCAGC GCCAGTTTCC GCCACATGTC TTTGCTTGAT	1560
ATCTCTTCCG ATCTGGCCAC GGACCACTTG CTGGGCTGTG ATCTGTCTAT TGCTTCAAAA	1620
CACATCAGCA AACCTGTGCA AGAACCTCTG GTGCTGCCTG AGGTCTTTGG CAACTTGAAC	1680
TCTGTCATGT GTGTGGAGGG TGAAGCTGGA AGTGGAAGA CGGTCCTCCT GAAGAAAATA	1740
GCTTTTCTGT GGGCATCTGG ATGCTGTCCC CTGTAAACA GGTTCCAGCT GGTTTTCTAC	1800
CTCTCCCTTA GTTCCACCAG ACCAGACGAG GGGCTGGCCA GTATCATCTG TGACCAGCTC	1860
CTAGAGAAAG AAGGATCTGT TACTGAAATG TGCATGAGGA ACATTATCCA GCAGTTAAAG	1920
AATCAGGTCT TATTCCTTTT AGATGACTAC AAAGAAATAT GTTCAATCCC TCAAGTCATA	1980
GGAAACTGA TTCAAAAAA CCACTTATCC CGGACCTGCC TATTGATTGC TGTCCGTACA	2040
AACAGGGCCA GGGACATCCG CCGATACCTA GAGACCATTG TAGAGATCAA AGCATTTCCTC	2100
TTTTATAATA CTGTCTGTAT ATTACGGAAG CTCTTTTCAC ATAATATGAC TCGTCTGCGA	2160
AAGTTTATGG TTTACTTTGG AAAGAACCAA AGTTTGCAGA AGATACAGAA AACTCCTCTC	2220
TTTGTGGCGG CGATCTGTGC TCATTGGTTT CAGTATCCTT TTGACCCATC CTTTGATGAT	2280
GTGGCTGTTT TCAAGTCCTA TATGGAACGC CTTTCCTTAA GGAACAAAGC GACAGCTGAA	2340
ATTCTCAAAG CAACTGTGTC CTCCTGTGGT GAGCTGGCCT TGAAAGGGTT TTTTTCATGT	2400
TGCTTTGAGT TTAATGATGA TGATCTCGCA GAAGCAGGGG TTGATGAAGA TGAAGATCTA	2460
ACCATGTGCT TGATGAGCAA ATTTACAGCC CAGAGACTAA GACCATTCTA CCGGTTTTTA	2520
AGTCCTGCCT TCCAAGAATT TCTTGCGGGG ATGAGGCTGA TTGAACTCCT GGATTGAGAT	2580
AGGCAGGAAC ATCAAGATTT GGGACTGTAT CATTTGAAAC AAATCAACTC ACCCATGATG	2640
ACTGTAAGCG CCTACAACAA TTTTTTGAAC TATGTCTCCA GCCTCCCTTC AACAAAAGCA	2700
GGGCCCAAAA TTGTGTCTCA TTTGCTCCAT TTAGTGGATA ACAAAGAGTC ATTGGAGAAT	2760
ATATCTGAAA ATGATGACTA CTAAAGCAC CAGCCAGAAA TTCACTGCA GATGCAGTTA	2820
CTTAGGGGAT TGTGGCAAAT TTGTCCACAA GCTTACTTTT CAATGGTTTC AGAACATTTA	2880
CTGGTTCTTG CCCTGAAAAC TGCTTATCAA AGCAAACTG TTGCTGCGTG TTCTCCATTT	2940
GTTTTGCAAT TCCTTCAAGG GAGAACACTG ACTTTGGGTG CGCTTAACTT ACAGTACTTT	3000
TTCGACCACC CAGAAAGCTT GTCATTGTTG AGGAGCATCC ACTTCCCAAT ACGAGGAAAT	3060

0930338.07.10.1

AAGACATCAC CCAGAGCACA TTTTTCAGTT CTGGAAACAT GTTTTGACAA ATCACAGGTG 3120
 CCAACTATAG ATCAGGACTA TGCTTCTGCC TTTGAACCTA TGAATGAATG GGAGCGAAAT 3180
 TTAGCTGAAA AAGAGGATAA TGTAAGAGC TATATGGATA TGCAGCGCAG GGCATCACCA 3240
 GACCTTAGTA CTGGCTATTG GAAACTTTCT CCAAAGCAGT ACAAGATTCC CTGTCTAGAA 3300
 GTCGATGTGA ATGATATTGA TGTGTAGGC CAGGATATGC TTGAGATTCT AATGACAGTT 3360
 TTCTCAGCTT CACAGCGCAT CGAACTCCAT TTAAACCACA GCAGAGGCTT TATAGAAAGC 3420
 ATCCGCCCAG CTCTTGAGCT GTCTAAGGCC TCTGTCACCA AGTGCTCCAT AAGCAAGTTG 3480
 GAACTCAGCG CAGCCGAACA GGAAGTCTT CTCACCCTGC CTTCCCTGGA ATCTCTTGAA 3540
 GTCTCAGGGA CAATCCAGTC ACAAGACCAA ATCTTTCCTA ATCTGGATAA GTTCCTGTGC 3600
 CTGAAAGAAC TGTCTGTGGA TCTGGAGGGC AATATAAATG TTTTTCAGT CATTCTGAA 3660
 GAATTTCCAA ACTTCCACCA TATGGAGAAA TTATTGATCC AAATTTCAGC TGAGTATGAT 3720
 CCTTCCAAAC TAGTAAATT AATTCAAAT TCTCCAAACC TTCATGTTTT CCATCTGAAG 3780
 TGTAAGTTCT TTTGGGATTT TGGGTCTCTC ATGACTATGC TTGTTTCCTG TAAGAACTC 3840
 ACAGAAATTA AGTTTTCGGA TTCATTTTTT CAAGCCGTCC CATTTGTTGC CAGTTTGCCA 3900
 AATTTTATTT CTCTGAAGAT ATTAAATCTT GAAGGCCAGC AATTTCTGA TGAGGAAACA 3960
 TCAGAAAAAT TTGCCTACAT TTTAGGTTCT CTTAGTAACC TGAAGAATT GATCCTTCCT 4020
 ACTGGGGATG GAATTTATCG AGTGGCCAAA CTGATCATCC AGCAGTGTC GCAGCTTCAT 4080
 TGTCTCCGAG TCCTCTCATT TTTCAAGACT TTGAATGATG ACAGCGTGGT GGAAATTGCC 4140
 AAAGTAGCAA TCAGTGGAGG TTTCCAGAAA CTTGAGAACC TAAAGCTTTC AATCAATCAC 4200
 AAGATTACAG AGGAAGGATA CAGAAATTC TTTCAAGCAC TGGACAACAT GCCAACTTG 4260
 CAGGAGTTGG ACATCTCCAG GCATTTTACA GAGTGTATCA AAGCTCAGGC CACAACAGTC 4320
 AAGTCTTTGA GTCAATGTGT GTTACGACTA CCAAGGCTCA TTAGACTGAA CATGTTAAGT 4380
 TGGCTCTTGG ATGCAGATGA TATTGCATTG CTTAATGTCA TGAAAGAAAG ACATCCTCAA 4440
 TCTAAGTACT TAACTATTCT CCAGAAATGG AACTGCGGT TCTCTCCAAT CATTGAGAAA 4500
 TAAAAGATTC AGCTAAAAAC TGCTGAATCA ATAATTTGTC TTGGGGCATA TTGAGGATGT 4560
 AAAAAAGTT GTTGATTAAT GCTAAAAACC AAATTATCCA AAATTATTTT ATTAATATT 4620
 GCATACAAAA GAAATGTGT AAGGCTTGCT AAAAAACAAA ACAAACAAA ACACAGTCCT 4680
 GCATACTCAC CACCAAGCTC AAGAAATAAA TCATCACCAA TACCTTTGAG GTCCTGAGT 4740

AATCCACCCC AGCTAAAGGC AAACCCTTCA ATCAAGTTTA TACAGCAAAC CCTCCATTGT 4800
 CCATGGTCAA CAGGGAAGGG GTTGGGGACA GGTCTGCCAA TCTATCTAAA AGCCACAATA 4860
 TGAAGAAGT ATTCAATTTA TATAATAAAT GGCTAACTTA ACGGTTGAAT CACTTTTCATA 4920
 CATGGATGAA ACGGGTTTAA CACAGGATCC ACATGAATCT TCTGTGGGCC AAAATATGTT 4980
 CCTTAATCCT TGTAGAACCT GTCTTCTATA TTGAACTAGC TTTGGTACAG TAGAGTTAAC 5040
 TTACTTTCCA TTTATCCACT GCCAATATAA AGAGGAAACA GGGGTTAGGG AAAAATGACT 5100
 TCATTCCAGA GGCTTCTCAG AGTTCAACAT ATGCTATAAT TTAGAATTTT CTTATGAATC 5160
 CACTCTACTT GGGTAGAAAA TATTTTATCT CTAGTGATTG CATATTATTT CCATATCATA 5220
 GTATTTTCATA GTATTATATT TGATATGAGT GTCTATATCA ATGTCAGTGT CCAGAATTC 5280
 GTTCCTACCA GTTGAGTAGT TTTCTGAACG GCCAGAAGAC CATTGGAAT TCATGATACT 5340
 ACTATAAGTT GGTAAACAAC CATACTTTTA TCCTCATTTT TATTCTCACT AAGAAAAAAG 5400
 TCAACTCCCC TCCCCTTGGC CAAGTATGAA ATATAGGGAC AGTATGTATG GTGTGGTCTC 5460
 ATTTGTTTAG AAAACCACTT ATGACTGGGT GCGGTGGCTC ACACCTGTAA TCCCAGCACT 5520
 TTGGGAGGCT GAGGCGGGCG AATCATTTGA GGTGAGGAGT TCGAGACCGG CCTGGCCAGC 5580
 ATGGTGAAAC CCCATTTTTG CTAAAGGTAC AAAAATTAGC CAGGTGTGGT GGCACATGCC 5640
 TGTGGTCCCA GCCACTGGGG CGGCTGAGAC GCAGGACTTG CTTGAACCCG GGAGGCAGAG 5700
 GTTGCACTGA GCCGAGATGG CGCCACTGCA TTCCAGCCTG GGCAACAGAG CAAGACCCTG 5760
 TCTGTTTCAA AACAAAAAAC AAAACCACTT ATATTGCTAG CTACATTAAG AATTTCTGAA 5820
 TATGTTACTG AGCTTGCTTG TGGTAACCAT TTATAATATC AGAAAGTATA TGTACACCAA 5880
 AACATGTTGA ACATCCATGT TGTACAACCTG AAATATAAAT AATTTTGTCA ATTATACCTA 5940
 AATAAACTG GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 5984

09030330.07.10.1